

Bet v 1 sense	5′-	${\tt AATTATGAGACTGAGACC\underline{A}CCTCTGTTATCCCAGCAGCTCG}$	-3
Bet v 1 non-sense	3'-	${\tt TTAATACTCTGACTCTGG\underline{T}GGAGACAATAGGGTCGTCGAGC}$	-5
sense primer	5'-	TGAGACC <u>C</u> CCTCTGTTATCCCAG	<b>-3</b>
non-sense primer	31-	ATACTCTGACTCTGGGGGGGACA	-5

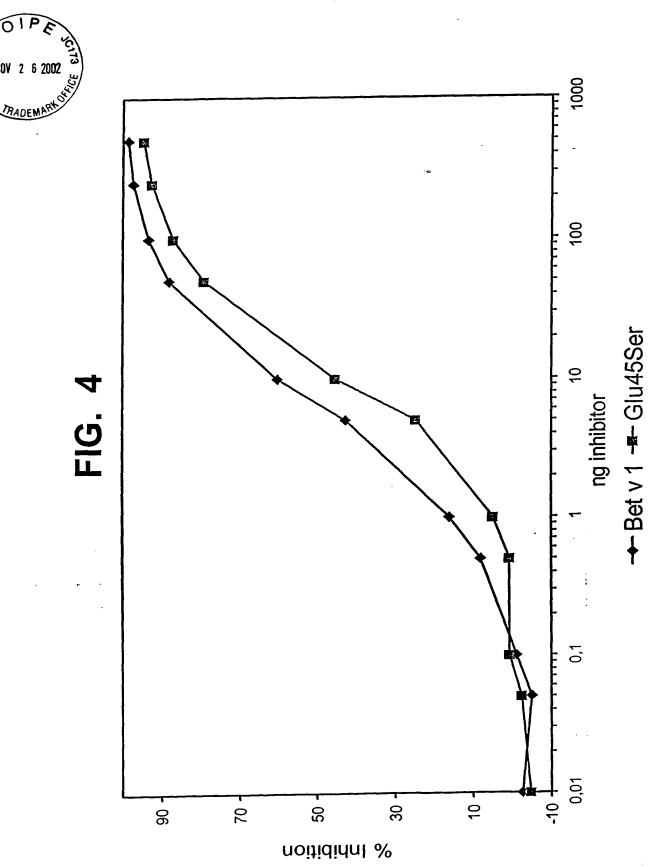


all	sense	1: 183Bv, 15-mer 5'-GTTGCCAACGATCAG
1	sense	2: 184Bv, 23-mer 5'-TGAGACCCCCTCTGTTATCCCAG
1	non-sense	3: 185Bv, 23-mer 5'-ACAGAGGGGGTCTCAGTCTCATA
2	sense	4:186Bv, 31-mer 5'-GATACCCTCTTTCCACAGGTTGCACCCCAAG
2	non-sense	5: 187Bv, 31-mer 5'-ACCTGTGGAAAGAGGGTATCGCCATCAAGGA
3	sense	6: 188Bv, 23-mer 5'-AACATTTCAGGAAATGGAGGCC
3	non-sense	7: 189Bv, 23-mer 5'-TTTCCTGAAATGTTTTCAACACT
4	sense	8: 190Bv, 23-mer 5'-TTAAGAACATCAGCTTTCCCGAA
4	non-sense	9: 191Bv, 23-mer 5'-AGCTGATGTTCTTAATGGTTCCA
5	sense	10: 192Bv, 23-mer 5'-GGACCATGCAAACTTCAAATACA
5	non-sense	11: 193Bv, 23-mer 5'-AGTTTGCATGGTCCACCTCATCA
6	sense	12: 194Bv, 23-mer 5'-TTTCCCTCAGGCCTCCCTTTCAA
6	non-sense	13: 195Bv, 23-mer 5'-AGGCCTGAGGGAAAGCTGATCTT
7	sense	14: 196Bv, 24-mer 5'-TGAAGGATCTGGAGGGCCTGGAAC
7	non-sense	15: 197Bv, 24-mer 5'-CCCTCCAGATCCTTCAATGTTTTC
8	sense	16: 198Bv, 24-mer 5'-GGCAACTGGTGATGGAGGATCCAT
8	non-sense	17: 199Bv, 24-mer 5'-CCATCACCAGTTGCCACTATCTTT
all	non-sense	18: 200Bv, 15-mer 5'-CATGCCATCCGTAAG

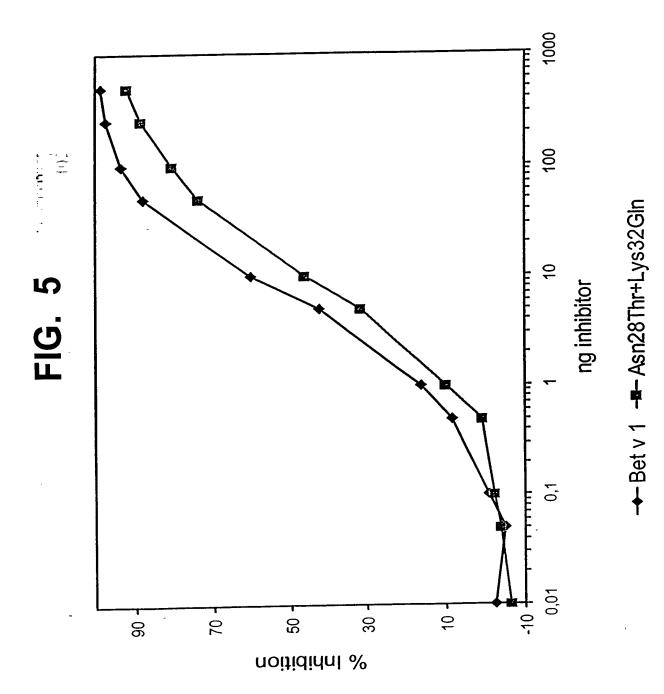


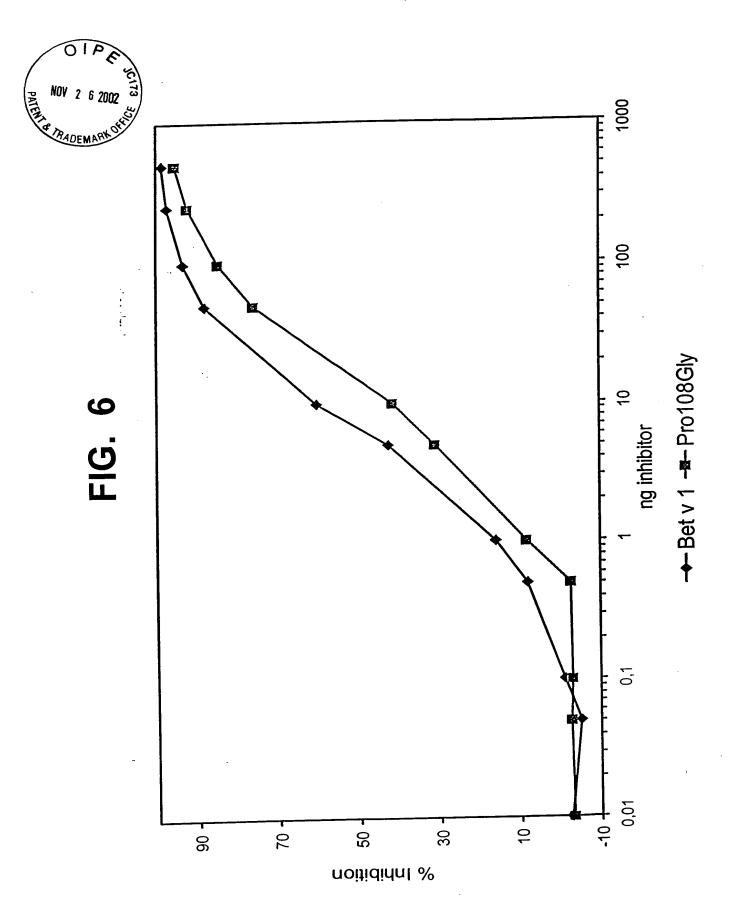
									1 (7	Y-C	}									
GG'	rgtv	GTT	raa'	TTAT	'GA	GAC	rga(	ac	CĀC	TC	TGTI	TAT	CCC.	AGC	AGC	TCG	ACT	GTT	CAAG	60
G	v	F	N	Y	E	т	E	Т	T-1	s	v	r	P	A	A	R	L	F	ĸ	20
			:	9 (A-	G)		2 (	A-6	C) 2	(A	-C)									
GCC	TT	PTATO	CT.	IG <u>A</u> T	GG	GA7	7 <u>4</u> 47	CT(	CTTT	CCI	A <u>A</u> AG	GTI	rgcz	ACCC	CA	AGC	CAT	rag	CAGT	120
A	F	I	L	D-G	G	D	N-T	, F	F	P	K-Q	V	A	P	Q	A	I	s	s	40
		3 (G	A-7	rc)	7	7 (AA	-TC	)					4	(G-C	:)		6	(GA	-TC)	
GTI	GAA	AAC	'ATT	<u>rga</u> a	GGJ	L <u>aa</u> t	'GGA	GGC	CCT	GG?	ACC	ATT	'AAG	AAG	ΣΥΛ	CAGO	TT	rcc	<u>GA</u> A	180
v	E	N	1	E-S	G	N-S	G	G	P	G	T	I	K	K-N	I	s	F	P	E-S	60
															9	(C#	Y-TC	;)		
GGC	CTC	CCT	TTC	'AAG'	rac	GTG	AAG	GAC	AGA	GTI	'GAT	GAG	GTG	GAC	CAC	<u>'A</u> CA	AAC	TTC	AAA	240
G	L	P	F	K	Y	v	K	D	R	v	D	E	v	D	H	T-A	N	F	K	80
TAC	AAT	TAC	AGC	GTG/	ATC	GAG	GGC	GG1	ccc	ATA	.GGC	GAC	ACA	TTG	GAG	AAG	ATC	TCC	AAC	300
Y	N	Y	s	v	I	E	G	G	P	I	G	D	T	L	E	K	I	s	N	100
<u>GAG</u>	ATA	AAG	ATA	GTG0	CA	AC <u>C</u>	CCIV	GAT	GGA	3GA	TCC	ATC	TTG	AAG.	ATC	AGC	AAC	AAG	TAC	360
E	1	K	I	v	A	T	P-G	D	.G	G	s	1.	L	ĸ	I	s	N	K	Y	120
																			GGC	
Н	Т	ĸ	G	D	Н	E	v	K	A	Е	Q	v	ĸ	A	s	K	E	M	G.	140
																				•
GAG.	ACA	CTT	TTG	AGGC	CC	GTT	GAG	AGC	TAC	CTC	TTG	GCA(	CAC	TCC	GAT	GCC	TAC	AAC	TAA	480
E	т	L	L	R	A	v	E	s	Y	L	L	A	н	s	D	A	Y	N	stop	159



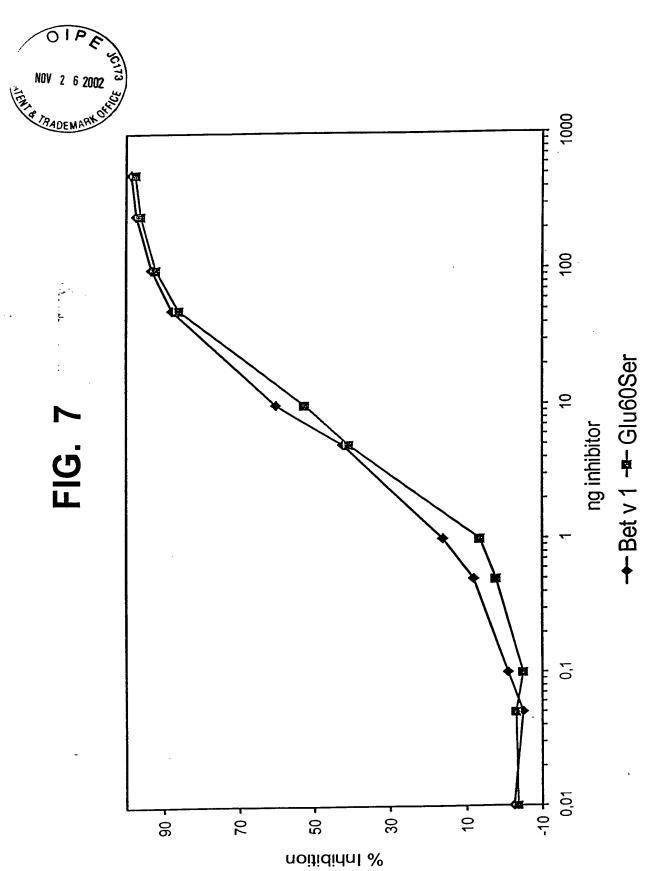


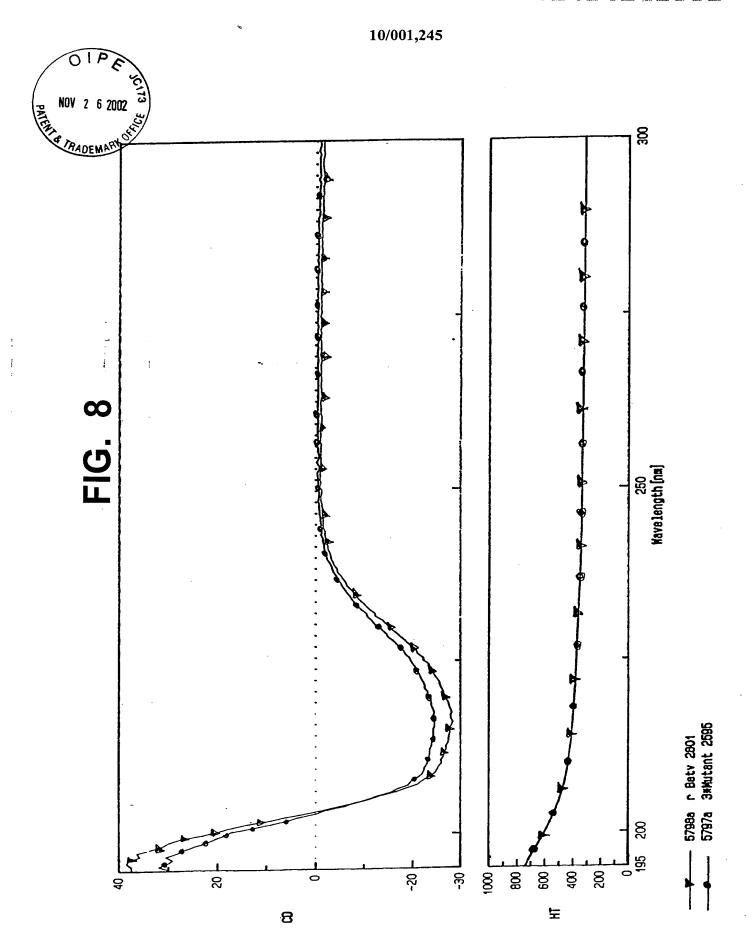


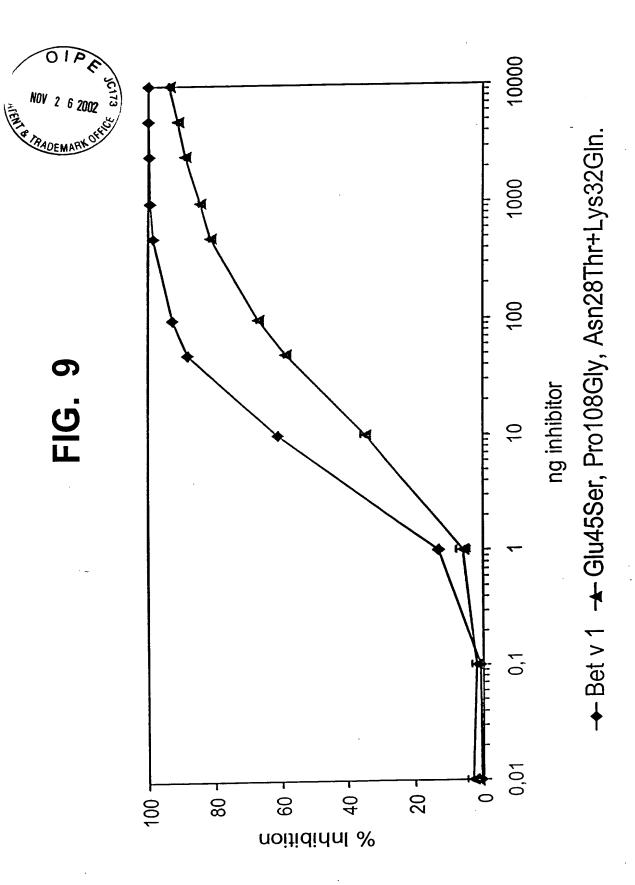






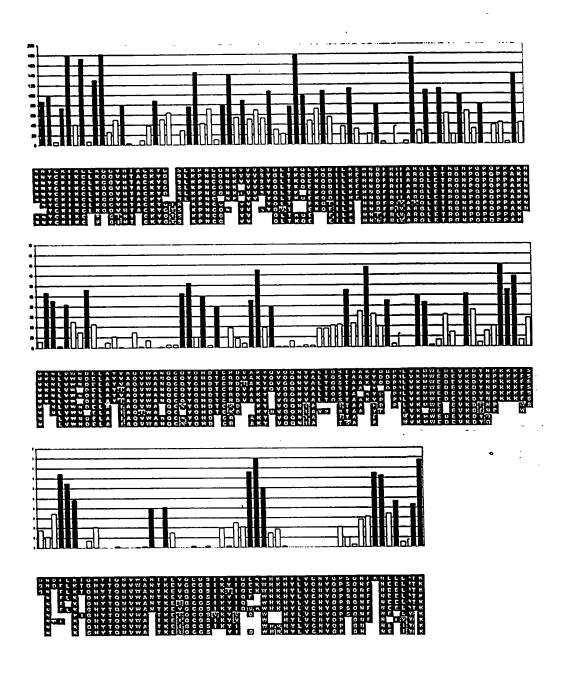






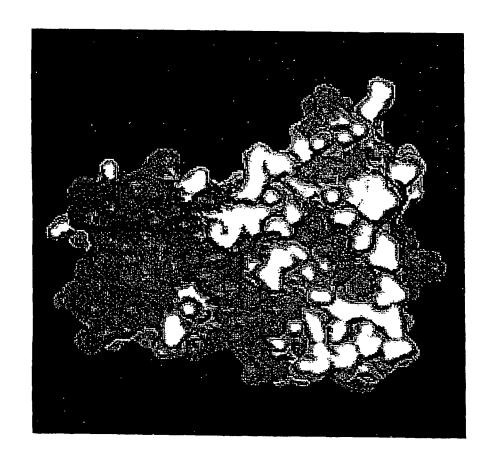


## FIG. 10 A





# FIG. 10 B





## FIG. 11 A

Ves v 5 mutant 1 (K72A)

Ves v 5 sense	5´- AC	CACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGA	-3 ^
Ves v 5 non-sense	3 ~ TG	GTGTCGGAGGTCGCTTCTTATACTTTTTAAACCATACCT	-5´
sense primer	5´~	CCAGCG <u>GCT</u> AATATGAAAAAT	-31
non-sense primer	3 -	GTCGGAGGTCGCCGATTATAC	-51

## FIG. 11 B

Ves v 5 mutant 2 (Y96A)

Ves v 5 sense	5′-	${\tt GGCTAATCAATGTCAATATGGTCACGATACTTGCAGGGATG}$	-3 ~
Ves v 5 non-sense	3 -	${\tt CCGATTAGTTACAGTTATACCAGTGCTATGAACGTCCCTAC}$	-5´
sense primer	5′-	TGTCAA <u>GC</u> TGGTCACGATACT	-3^
non-sense primer	3 -	TTAGTTACAGTT <u>CG</u> ACCAGTG	-5′

## FIG. 12

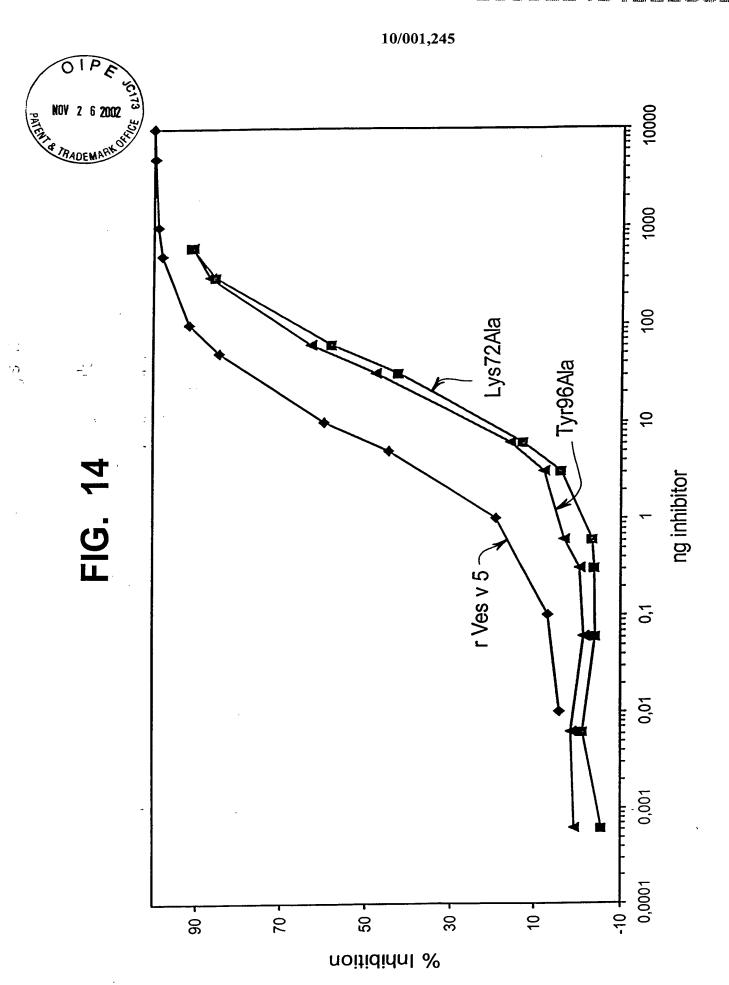
all sense 1: XhoI start, 38-mer:

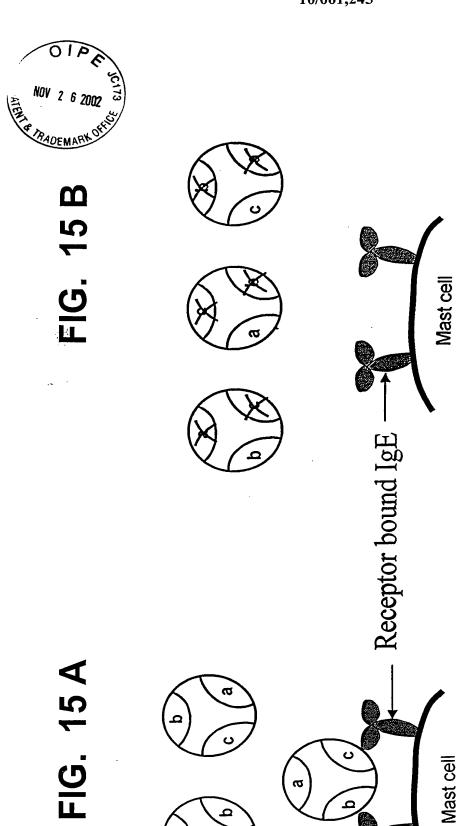
# ECORI 5'-CCGCTCGAGAAAAGAAACAATTATTGTAAAATAAAATG L E K R N N Y C K I K Kex2 cleavage site amino terminus of Ves v 5

1	sense	1: K72As	21-mer	5´-CCAGCGGCTAATATGAAAAAT
1	non-sense	2: K72Aa	21-mer	5´-CATATTAGCCGCTGGAGGCTG
2 2	sense	3: Y96As	21-mer	5 <sup>-</sup> -TGTCAAGCTGGTCACGATACT
	non-sense	4: Y96Aa	21-mer	5 <sup>-</sup> -GTGACCAGCTTGACATTGATT
all	non-sense	7: CT-pPI	CZαA, 21-mer	5`-ATTCATCAGCTGCGAGATAGG



1	AAC	CAA	CTA	rTG'	<b>TAA</b>	ATA	LAAA	ATG	rtt	JAAJ	AGG?	\GGT	rgt(	CA	rac:	rgco	CTG	CAA	ATA	rgga	60
1	N	N	Y	С	K	Į	K	С	L	K	G	G	V	Н	Т	A	С	ĸ	Y	G	20
61	AGT	CTT	LAA?	ACCO	GAAT	rtgo	CGG1	CAA1	CAA1	GT <i>I</i>	AGTO	GT <i>I</i>	ATCO	TAT	rggi	rct <i>i</i>	AACC	JAA!	CAA	AGAG	120
21	s	L	K	P	N	C	G	N	K	V	V	V	s	Y	G	L	T	K	Q	Е	40
121	AAA	CAA	GAC	CATO	TT.	AA	GAG	CAC	LAA:	GAC	TTT	AGA	CAA	LAA.	ATI	rgca	ACGF	AGGF	TTC	GAG	180
41	к	Q	D	1	L	K	E	H	N	D	F	R	Q	K	I	A	R	G	L	E	60
											999		K72					מחיים	TYC) C	יא ארי	240
181 61	ACT T	'AGA R	.GG1 G	raa: N	P	'GG <i>F</i> G	ACCA P	CAC Q	P	P	A	<u>aac</u> K	AA1 N	M	K	N	L	V	W	Ń	80
																				·GC)	
241	GAC	CAC	מיייני	ഭവ	<b>ጥ</b> ልጥ	<b>'</b> ርጥር	יניכי	ממטי	GTG	TGG	GCT	TAA	'CAA	TGT	CAA	_					300
81	D	E	L	A	Y	V	A	Q	V	W	A	N	Q	С	Q	Y	G	H	D	Ť	100
201	maa	x.a.a	CAT	איייא	מרא.	מממ	ጥለጥ	ሮክር	<b>Č</b> TT	ሊርል	ממי	מממ	ረሞ እ	GCC	מיזייני	ACA	GGT	'AGC	ACG	GCT	360
301	C	AGG D	GAI	GIM V	M N	AAA K	A.	CAG	V	G	0	N	v	A	L	т	G	s	Т	A	120
101	C	K	ט	v	Λ		•	¥	•	Ū	*	•	•			_					
261	COT	מממ	ጥልር	ሚልጥ	<u>የ</u> ደልጥ	רכש	ርጥጥ C	<b>44</b>	<b>ረ</b> ጥአ	GTT	ΑΑΑ	ATG	TGG	GAA	GAT	GAA	GTG	AAA	GAT	TAT	420
121	A	K	Y	D	D	P	v	K	L	v	ĸ	M	W	E	Ď	E	v	K	D	Y	140
															~~~	/	ma c	a com	~n n	አጥር፣	480
421	AAT	CCT	AAG	AAA	AAG	T-I-I	TCG	GGA	AAC	GAC	1.1.1.	CIG	AAA	ACC	ص ص	CAI	TAC	WC I	CAA	ATG M =	
141	N	P	K	K	K	F	S	G	N	ע	F	п	K	T	G	n	1	1	Q	14	100
481	GTT	TGG	GCT	AAC	ACC	AAG	GAA	GTT	GGT	TGT	GGA	AGT.	ATA	AAA	TAC	ATT	CAA	GAG	AAA	TGG	540
161	v	W	A	N	T	K	E	V	G	С	G	S	I	K	Y	I	Q	E	K	W	180
541	CAC	AAA	ሮልጥ	TAC	СТТ	GTA	TGT.	AAT	TAT	GGA	CCC.	AGC	GGA	AAC	TTT	AAG	AAT	GAG	GAA	CTT	600
181	Н	K	Н	Y	L	V	C	N	Y	G	P	s	G	N	F	ĸ	N	E	E	L	200
601	TAT	ממר	ልሮል	באמ	<b>ል</b> ልጥ																612
	IMI																				204





Cross-linking

No cross-linking



## FIG. 16 A

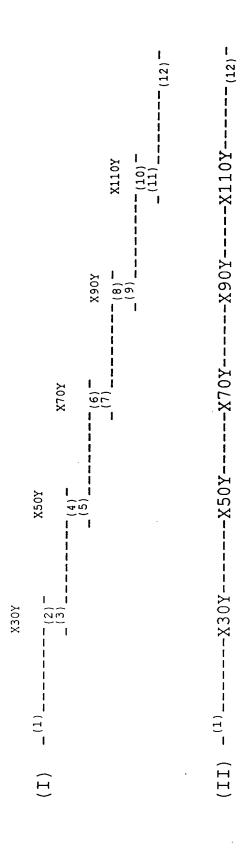
#### DNA SEQUENCE

#### ORIGIN

1	cacaaattct tctttcttcc ttactactga tcattaatct gaaaacaaaa ccaaacaaac
61	cattcaaaat gatgtacaaa attttgtgtc tttcattgtt ggtcgcagcc gttgctcgtg
121	atcaagtcga tgtcaaagat tgtgccaatc atgaaatcaa aaaagttttg gtaccaggat
181	gccatggttc agaaccatgt atcattcatc gtggtaaacc attccaattg gaagccgttt
241	tcgaagccaa ccaaaacaca aaaacgcta aaattgaaat caaagcctca atcgatggtt
301	tagaagttga tgttcccggt atcgatccaa atgcatgcca ttacatgaaa tgcccattgg
361	ttaaaggaca acaatatgat attaaatata catggaatgt tccgaaaatt gcaccaaaat
421	ctgaaaatgt tgtcgtcact gttaaagtta tgggtgatga tggtgttttg gcctgtgcta
481	ttgctactca tgctaaaatc cgcgattaaa tcaaacaaaa tttattgatt ttgtaatcac
541	aaatgattga ttttctttcc aaaaaaaaaa taaataaaat tttgggaatt c

## FIG. 16 B

1 <u>mmykilclsl lvaavar</u>dqv dvkdcanhei kkvlvpgchg sepciihrgk pfqleavfea 61 nqntktakie ikasidglev dvpgidpnac hymkcplvkg qqydikytwn vpkiapksen 121 vvvtvkvmgd dgvlacaiat hakird







## FIG. 18 A

331 pMalc (s)		•			
	189BV (a)				
	188BV (s)		_		
		362BV (a)			
		361BV (s			
			364BV (a)		
			363BV (s)		
				366BV (	<del>a)</del>
				365BV (	
					332pMalc (a)

## FIG. 18 B

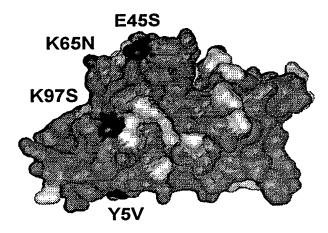
DNA templat	e: Bet v 1 (2571	1) carrying N28	BT, K32Q, P108G mutations
331pMalc			
	368BVa		
	367BVs		
		370BVa	
		369BVs	

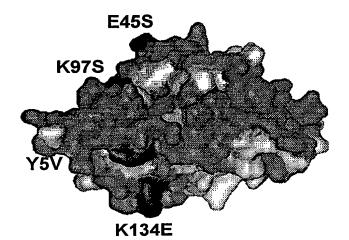
372BVa

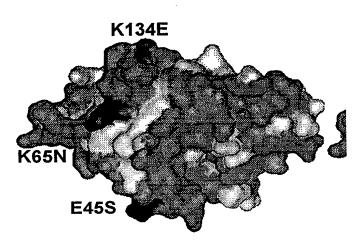


## FIG. 19 A

Bet v 1 (2628)



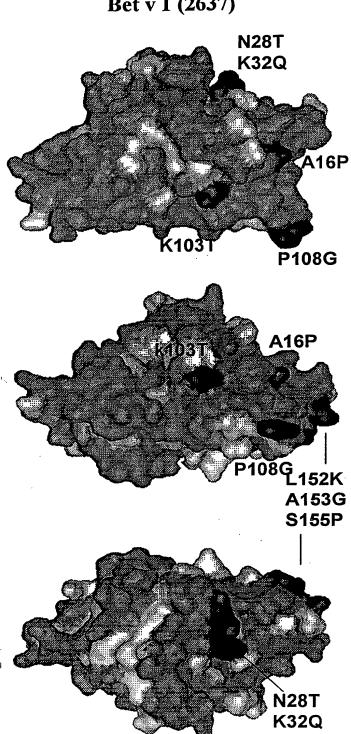




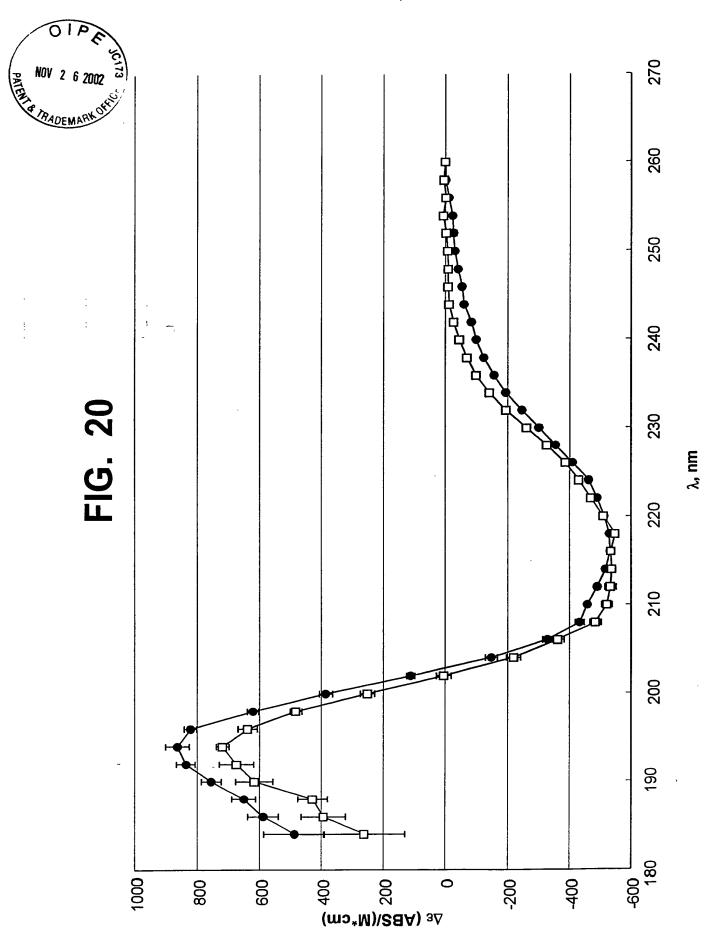


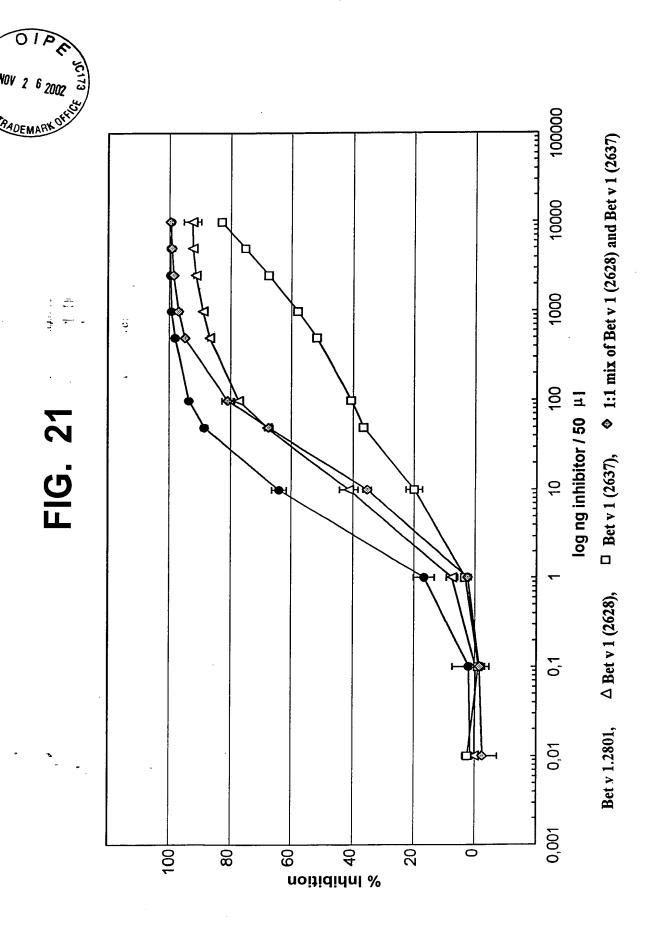
## FIG. 19 B

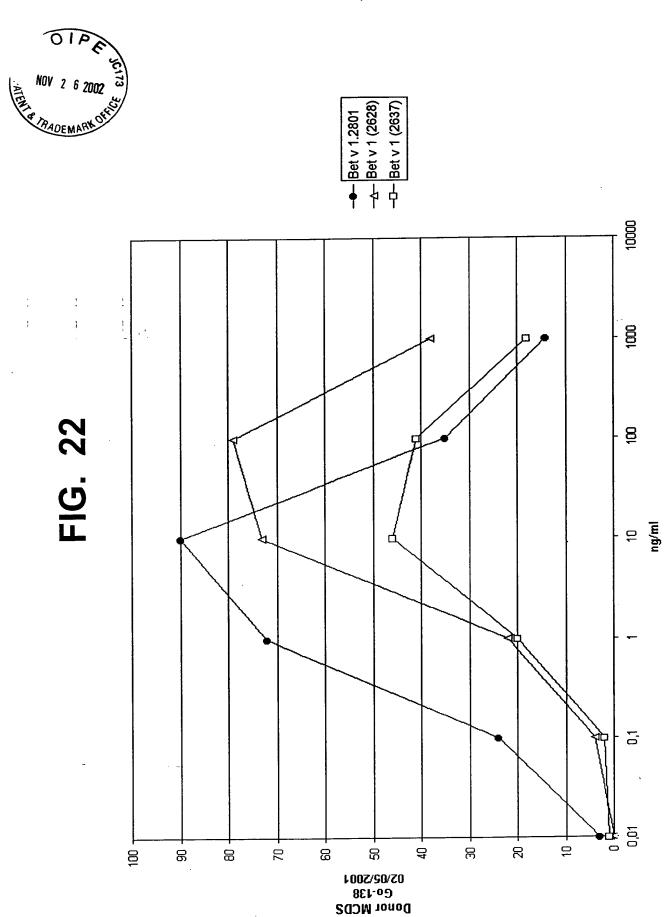
Bet v 1 (2637)



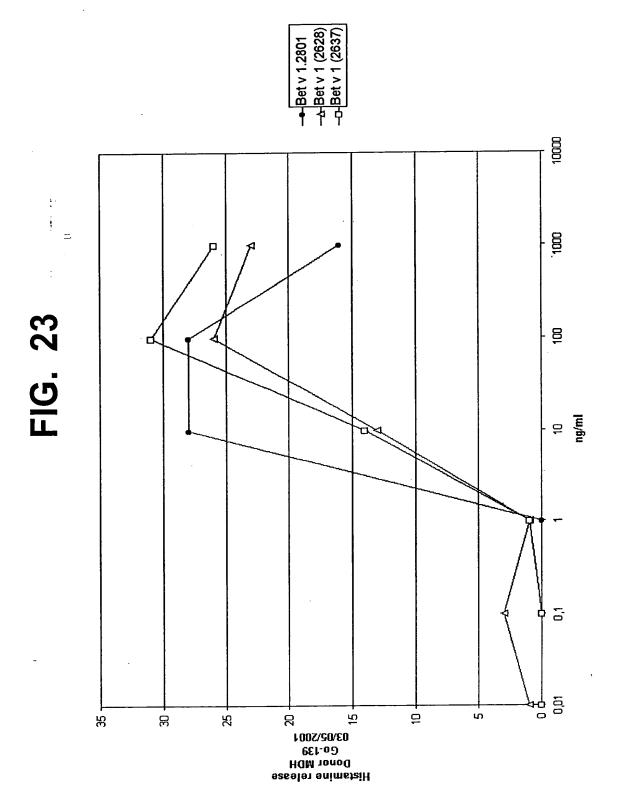


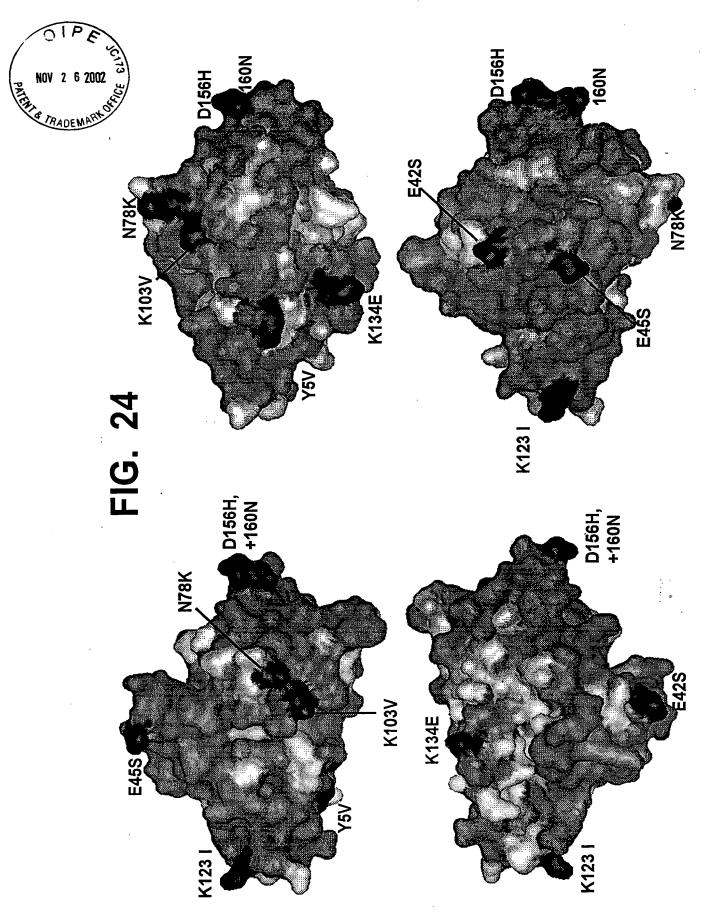


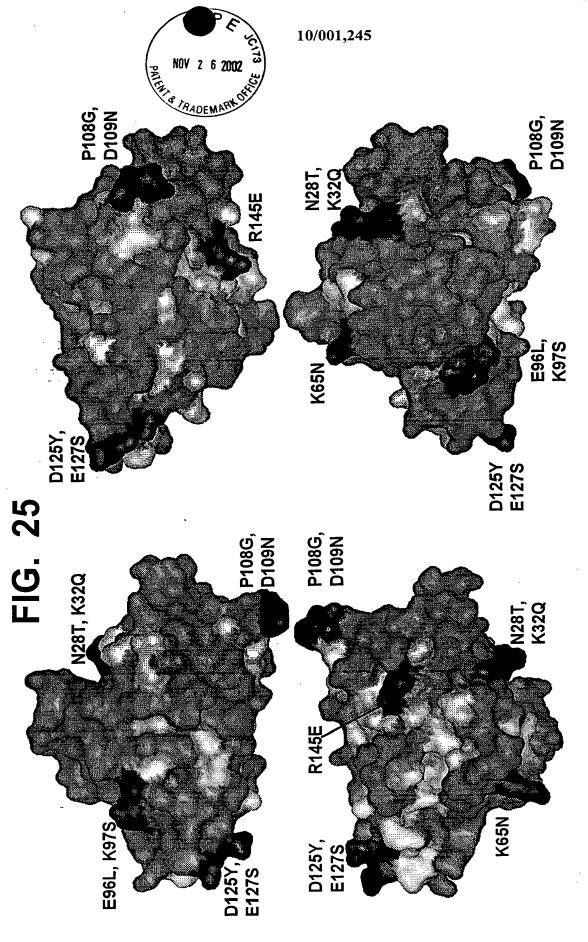


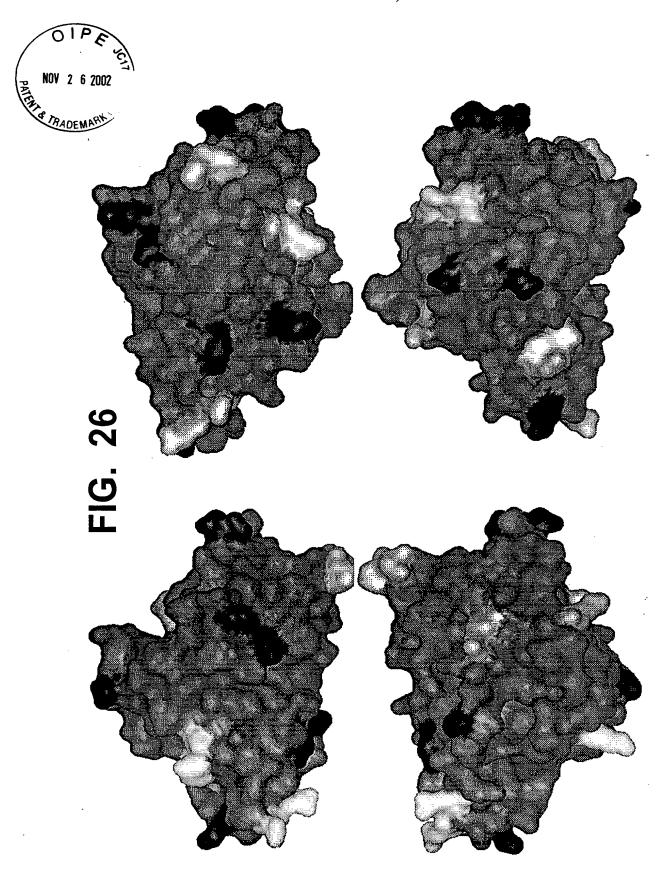


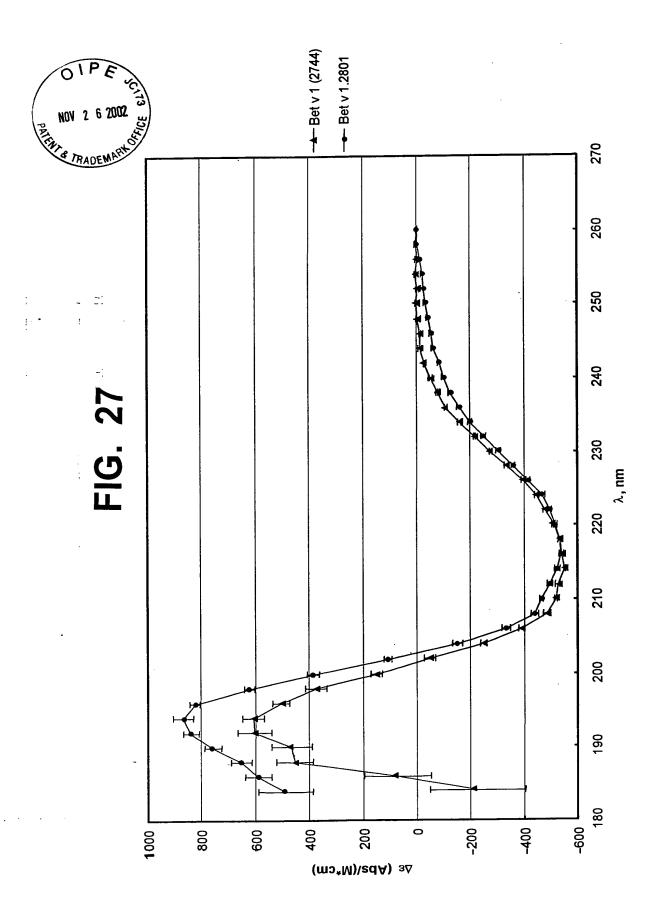
Histamine release

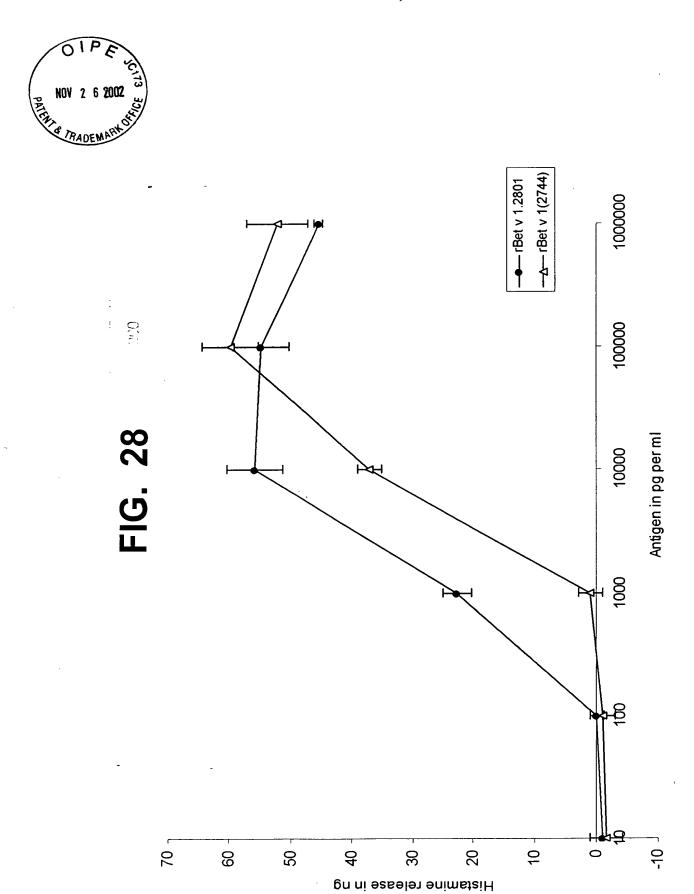


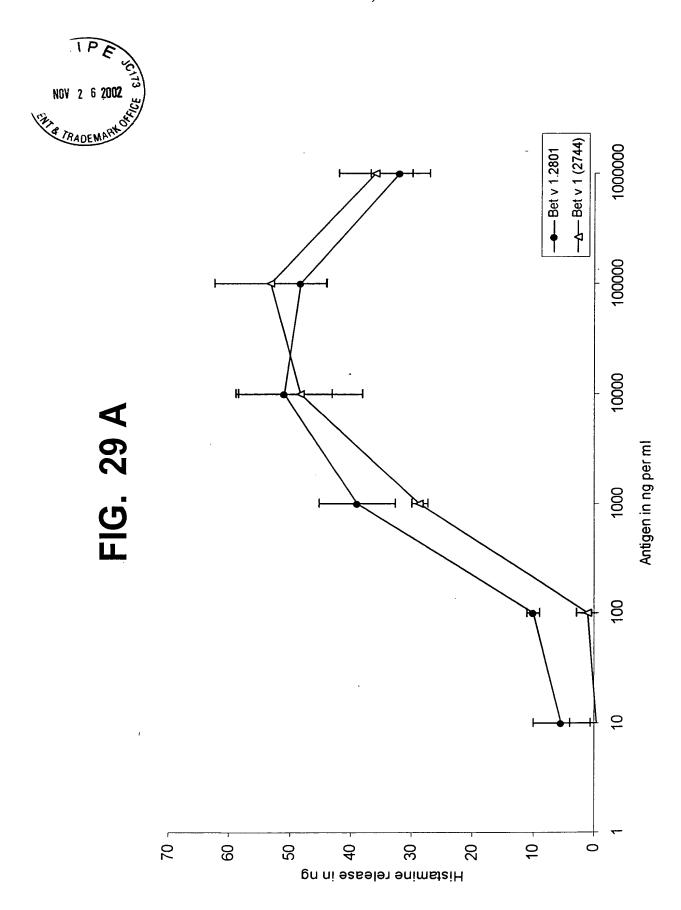












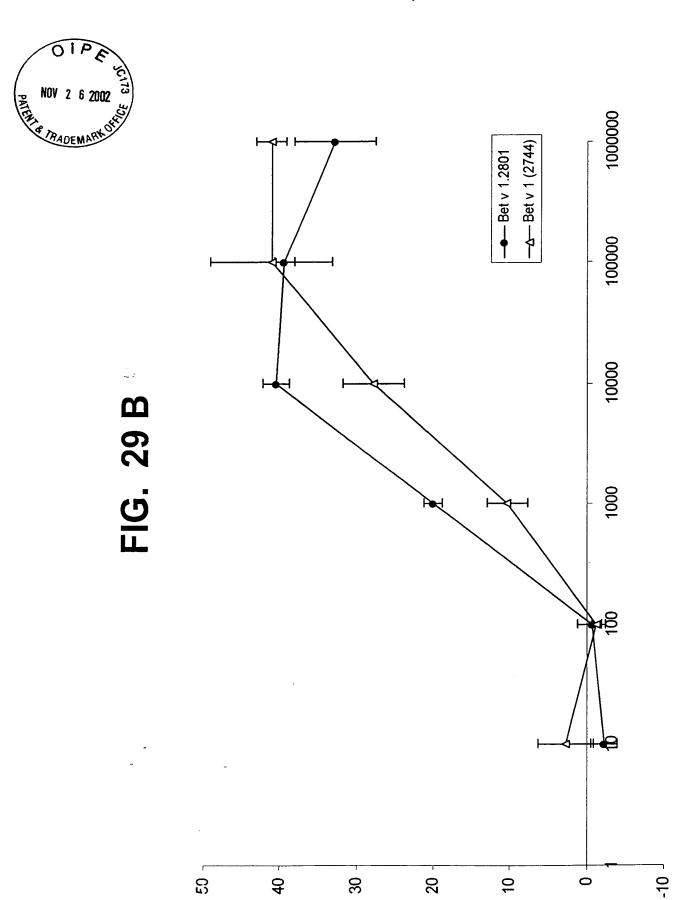
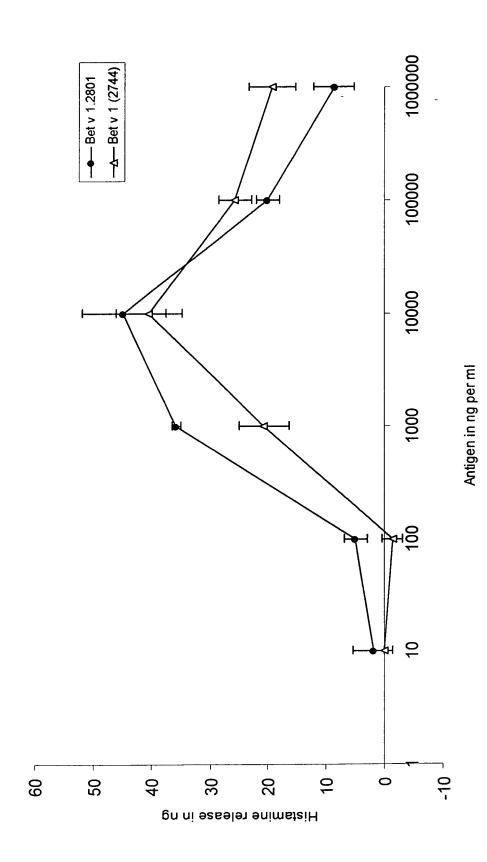
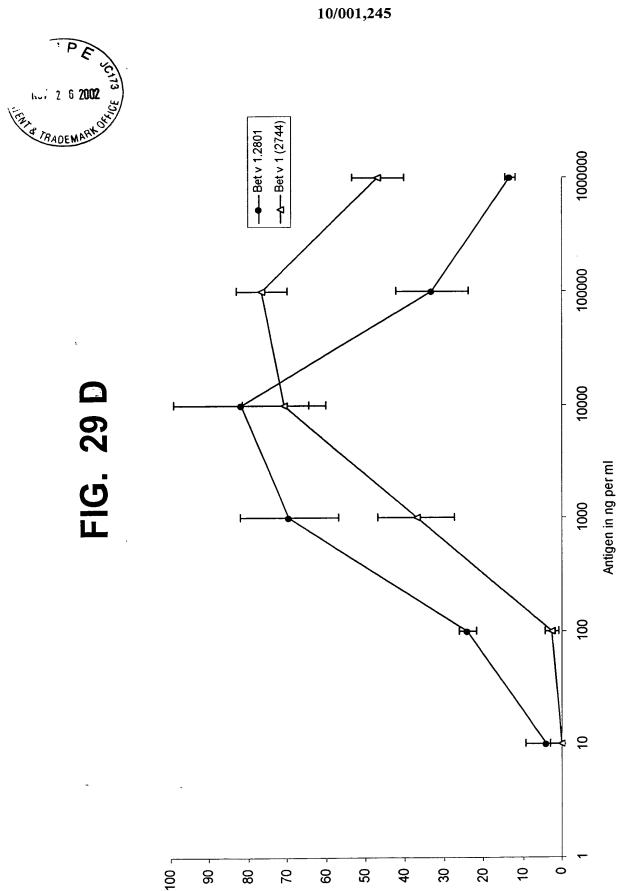


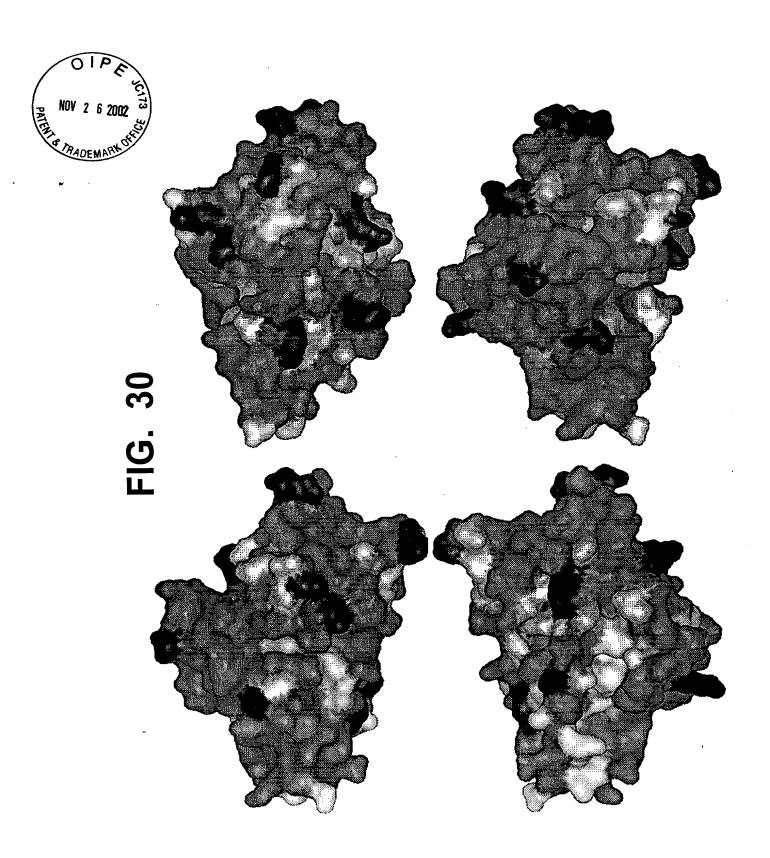


FIG. 29 C



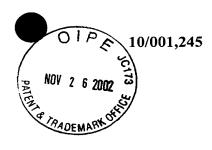


Histanine release in ng





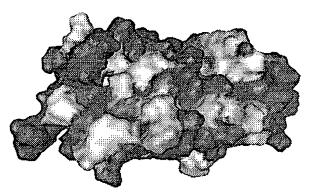
				Xho I
K6A	sense	OB43	42-mer	5' -CCGCTCGAGAAAAGAGATCAAGTCGATGTCGCCGATTGTGCC-3'
	anti-sense	OB28	39-mer	5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3'
K15E	sense	OB44	67-mer	Xho I 5' -CCG <u>CTCGAG</u> AAAAGAGATCAAGTCGATGTCAAAGATTGTGCC AACCATGAAATCAAAGAAGTTTTGG- 3'
	anti-sense	OB28	39-mer	Xba I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
H30N	sense	OB46	54-mer	Kpn I 5' -CGG <u>GGTACC</u> AGGATGTCATGGTTCAGAACCATGTATCATTAA CCGTGGTAAACC- 3'
	anti-sense	OB28	39-mer	Xba I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
E62S	sense	OB47	33-mer	5' -GCCTCAATCGATGGTTTATCAGTTGATGTTCCC- 3'
	anti-sense	OB48	33-mer	5' -GGGAACATCAACTGATAAACCATCGATTGAGGC-3'
H74N	sense	OB49	32-mer	5' -CATG <u>GCATGC</u> AATTACATGAAATGCCCATTGG- 3'
	anti-sense	OB28	39-mer	5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3'
K82N	sense	OB50	50-mer	Sph I 5'-CTACGCATGCCATTACATGAAATGCCCATTGGTTAATGGACAA CAATATG-3'
	anti-sense	OB28	39-mer	Xba I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3'

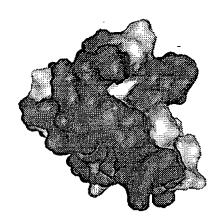


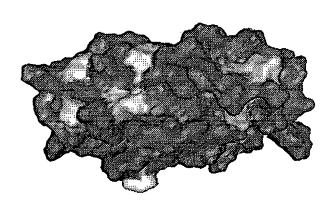
2 0		K V L V P G C H G S E P C L L K V L V P G C H G S E P C L L K S E P C L L L X V V V V V V V V V V V V V V V V	K K V L V P G C H G S E P C L - H K K V L V P G C H G S E P C L - H K K X M V D G C H G S D D C I - H K X M V D G C H G S D D C I - H K X M V D G C H G S D D C I - H K X M V D G C H G S D D C I - H K X M V D G C H G S D D C I - H K X M V D G C H G S D D C I - H K X M V D G C H G S D D C I - H		0 2	OVEG DPNACHYMKCPL	VPG-DPHACHYNKCP VPG-DPHACHYNKCP	VPG-DPNACHYMNCP VPG-DPNACHYMNCP	VPGIDPRACHYMKCP VPGIDINACHFMKCP	VPG-DT NACHFER CD		V P G I D N N I C F F W K C P	20000000000000000000000000000000000000
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FIG. 33







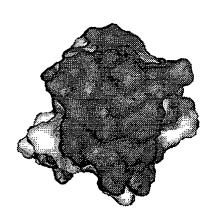
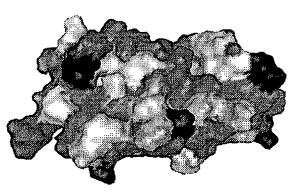
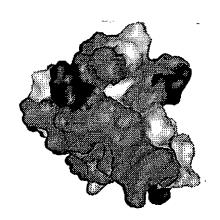
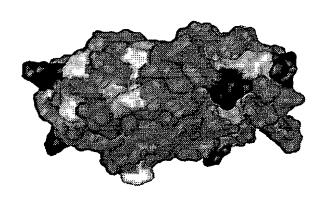


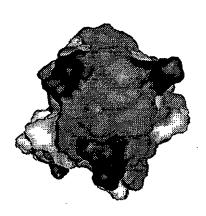


FIG. 34











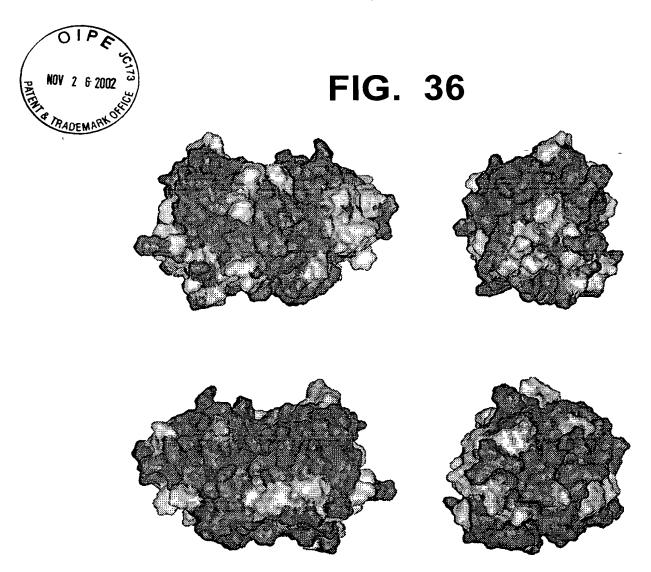
# FIG. 35 A

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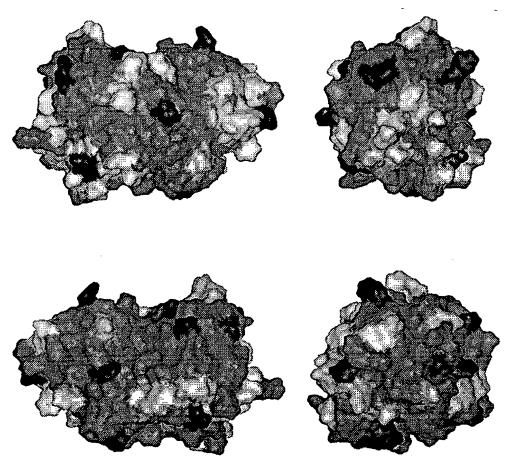
# FIG. 35 E

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0 8	T	P R G   F Y   Q Q M G V V   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S	.ļ	SALAVIIGINDEDAFRHY SALAVIIGINDEDAFRHY TAVAVIIGINDENAFRHY TAVAVIIGINDENAFRHY	A	2 0 0	WGDMGYGYFAAN - DIMM-	WGDNGYGYFAANINEHHIE	WG D H G Y G Y F A A Y I N L MM I E WG D H G Y G Y F A A X I N L MM I E E E	H H H H H H C A C L L H H H H H H H H H H H H H H H H H	WGDSGYGYROAGNN
0		P R G   F Y   Q Q M G V V   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S   R S	.ļ	A - A V - 1 G - K D L D A F R H Y A V A V - 1 G - K D L D A F R H Y A V A V - 1 G - K D L N A F R H Y A V A V - 1 G - K D L N A F R H Y	A	2 0 0	WGDMGYGYFAAN - DIMM-	WGDNGYGYFAANINEHHIE	GONGYGY FAAHINLEMIE GONGYGY FAAMINLEMIE	H H H H H H C A C L L H H H H H H H H H H H H H H H H H	WGDSGYGYROAGNN





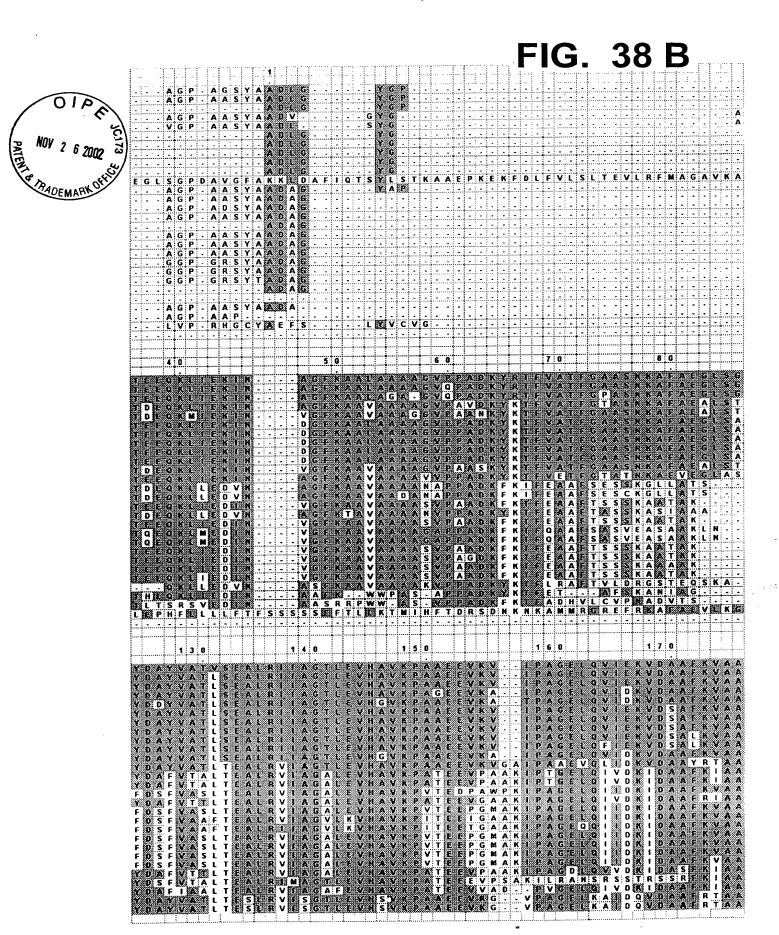
## FIG. 37



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A TRADEMARK	

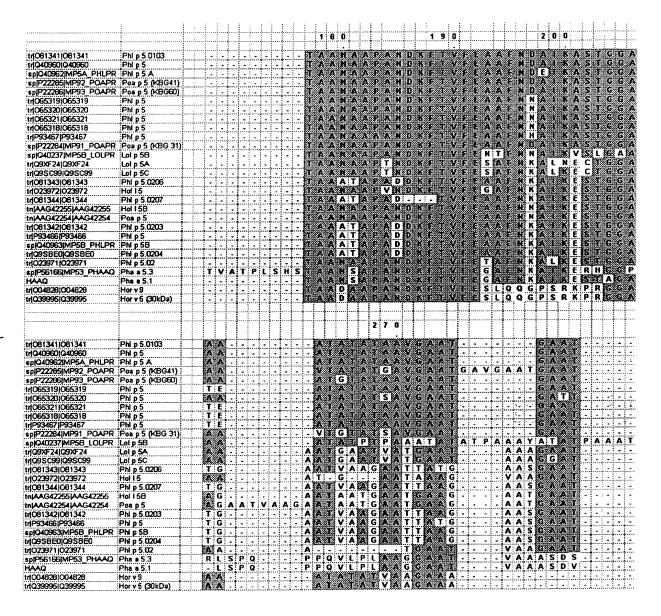
FIG. 38 A

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r/065320 065320 r/065321 065321	Phip 5 Phip 5		ļ.,		+:1		<u>.   -</u> .	H					H: -	:   :	<u> </u>			-	ŀ		-		:   :	1	-			:   :	†:
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r(P93467)P93467 sp(P22284)MP91_POAPR	Phi p 5 Poa p 5 (KBG 31)		<u>  :   .</u>		D		N	Ġ	ΑY	ĸ	T A	i.	K	Α Α	S	ĀV	Ā	P A	Ė	ĸ	F	PΝ	/ F	ò	Ā	T F	D	K N	i i
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rj081343 081343	Phl p 5.0206		1			M A	١V	Q	K Y	Ţ	٧,	L	F	LA	٧	A L	V						<u>.</u> .			.:			
rj023972 023972 rj081344 081344	Hol I 5 Phl p 5.0207		1:-	•	1:1	M A	٧V	Q	KY	Ť	V A	Ĺ	FI	LA	V	A L	٧	•						i	• 1				
n AAG42255 AAG42255	Hol I 58					M A	V	Q	KY	Ţ	VA	L	F	Ţ	V	A L	V		. <del> </del>		-	: .			-				
n AAG42254 AAG42254 n O81342 O81342	Poap 5 Phip 5.0203	s	V	KR	S	N G	S	\$ <del></del>	EV	н				PR	R	G P	R	- -	-		-				-	-   -		-   -	-
rjP93466 P93466 p Q40963 MP5B_PHLPR	Phl p 5		ļ <b>.</b>	-   -	4.4			ļļ.	-   -	À	 A A	A	V	PR		G P G P			<u> </u>								+-+		
Q9S8E0 Q8SBE0	Phi p 5.0204									L								- :	1.	- 1	:			İ.			•		1.
(1023971)023971 (ppp56166)MP53_PHAAQ	Phl p 5.02 Pha a 5.3		•	- -	<b> -</b>		v	à	KY	Ť	V A	i	F	A	M	AL	v		+-	-:		:   :	.   . <u></u> .			: :			
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1081341 081341	PN p 5.0103				100					A	C 4					A A	***	A G								ė.	G	K A	
r(Q40960)Q40960	PN p 5			:   . : . : .   . :	M		A	A			G Y			. 1			P	ΑE		-						e A		H A	
pjQ40962[MP5A_PHLPR pjP22286[MP92_POAPR	Phip 5 A Posp 5 (KBG41)	P	À	r L				A.			G X P A		G \	7						•	-				A	A A P		t A	anne.
p P22286 MP93_POAPR	Poap 5 (KBG60)	P		- [ -			A		L,A		P A	Α		/ 11	9		1	A G				:   :	1		A	<b>.</b>	-		
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pIP22284IMP91_POAPR	Pos p 5 (KBG 31)	Р	P	A S T P		F P			A		K V		A \	( ]	P	A A A T	P	A C A T	- P		•	-   -	<u>.</u>	A		P.S		K A K A	Ŧ
p Q40237 MP5B_LOLPR  Q9XF24 Q9XF24	Loi p 5A			T P	<b>36</b>	J.P							Ρ.,		Α	A T	P	ΑТ	Р	A	A	. , T			Α.	ΑG	G	K A	T
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pIQ40963 MP5B_PHLPR	PN p 58			-   -	<b></b>		.]]	Ξ.	- [	-	- 1	A							Ş				4-		Α.				W.
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1039995 039995	Hor v 5 (30kDa)		-	- -	╁┷╁			<b>.</b>	:   :		-   -	:-		-   -	ļ:	- <b>.</b>		-   -		÷	-  -	-   -		}				•	
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10813411081341	Phl p 5.0103	F		(		- 1		ŧ		9										H					Ē		Ţ	P E P E	A
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	Poa p 5 (KBG41)	E	2	( <b>6</b>					A S D S		N	I.V					A			ŀ	A A			A	Ē		Ŧ	P E P E	A
10653191065319	Phlp5		P	( 6			A	Ė	5 5	Š	K f	A	L	S	ĸ		A	A Y	ĸ	ï	٨			A	Ę.	G A	Ţ	P E	А
065320 065320  065321 065321	Phlp5 Phlp5	E	9	( G				Ē		9			ŀ.		ĸ	i	A	Ÿ	×	t	Ā		. +	Â	Ē	G A	Ť	P E	A
065318 065318	Phl p 5	E	P	4 6			A	ŧ.		S	K A	A	ı.	5	ĸ	, o	A	ΑY	ĸ	Ļ	۸.	1	Ţ	Ą	Ę.	G A	Ţ	PE	A
P93467 P93467  P22284 MP91_POAPR	Phi p 5 Poa p 5 (KBG 31)	E	P	K G		. 9	A	t v	BS AS	S	K A	P.	ŧ.	S	ĸ	Ö	Ä	ÂY	K	Ĺ	A.		S	À	Ē	G A	i	PE	A
piQ40237IMP5B_LOLPR	Lol p 5B			. 6	-	Y		D	- Q	5	K N			S		L D		ΑL	K	Ļ	A A	E	Ã	A	Q	G A G A	Ţ	P E	A
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1023972 023972 1081344 081344	Holl 5 Phip 5.0207								A P			G		/ P		L D	A	ΑY	S	V.	S				٧	G A		PΪ	A
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Q9SBE0 Q9SBE0	PM p 5.0204	1:		-1:					A P		-   -	G	W۱	/ P		Ö		a Y	S	V	A		Α		٧	G A		P.E	A
10239711023971 piP561661MP53_PHAAQ	Phi p 5.02 Pha a 5.3			+		· E	E	T I	K M K G	P		E	· .			Ď			S	v Ì	A I	ÑÑ			A		Ŧ	ΡĒ	A
AAQ	Pha a 5.1					- 6	(A)	Ť		P		Q	Œi	ΚA	Š	(E)			R	V	X.	∭ E	A			GS		PE	A
	Hor v 9	: -	A 1	7.44	Q	1 🍇	G	Q	c/me	en e	Mi	K	<b>.</b>	2 724	3 6 2	3 -		5 100	2000	8188	0 E.	₩.n	K	33A3	O	G A		P 6	(A)



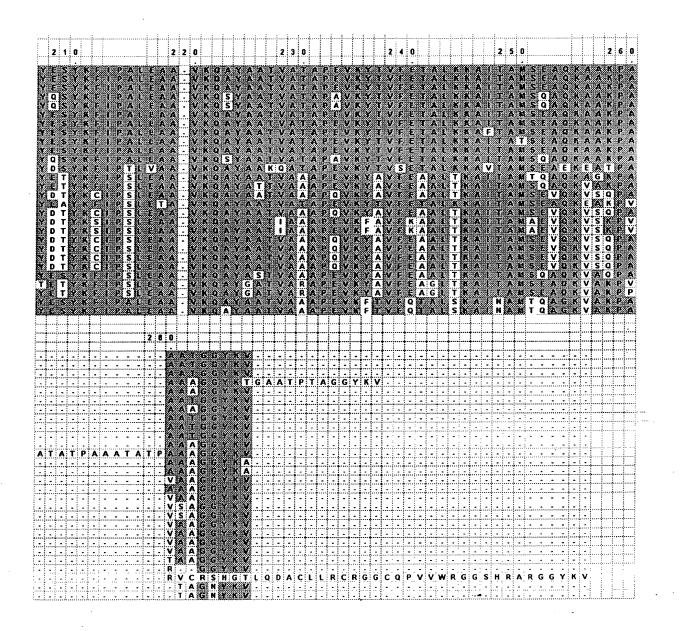


### FIG. 38 C



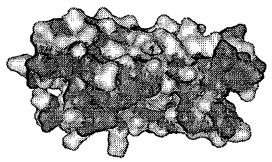


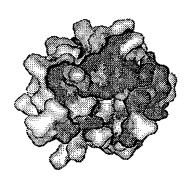
### FIG. 38 D

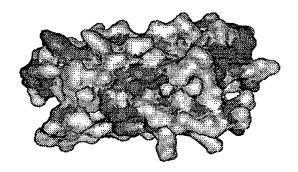


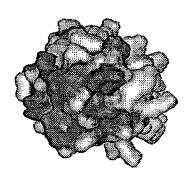


## FIG. 39 A



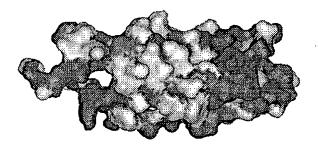


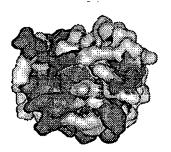


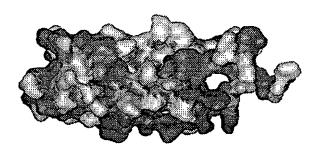


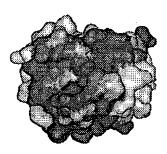


## FIG. 39 B



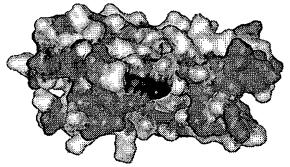


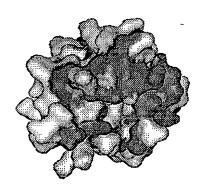


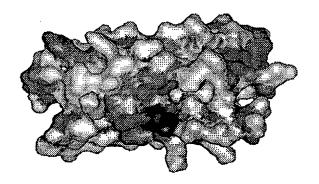


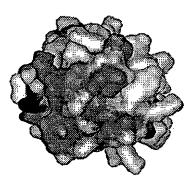


## FIG. 40 A



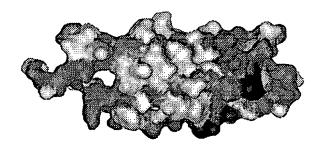


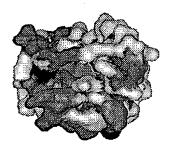


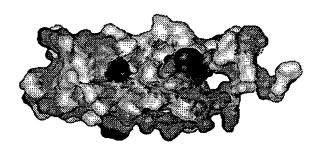


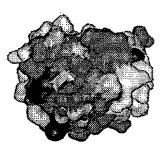


## FIG. 40 B

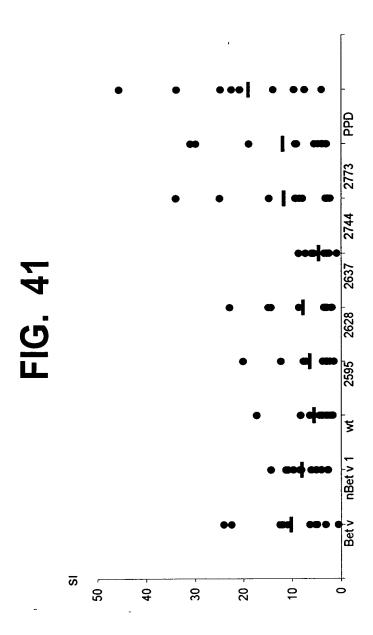






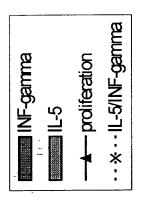






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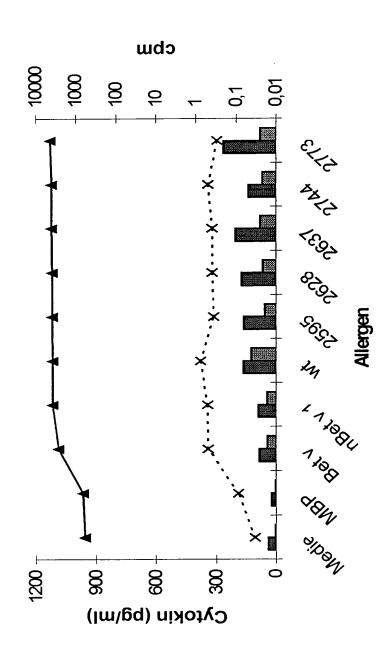
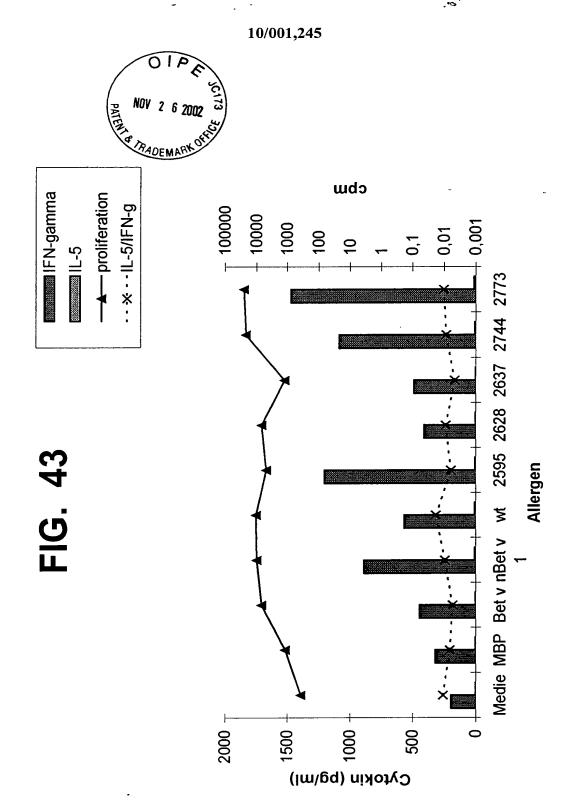


FIG. 42





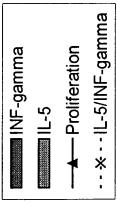


FIG. 44

